

Result No.	Score	Query	Match	Length	DB	ID	Description
1	27	96.4	45	6	5185254-1		Patent No. 5185254
2	27	96.4	265	4	US-08-413-805-2		Sequence 2, Appli
3	27	96.4	297	4	US-09-107-532A-4196		Sequence 4196, Ap
4	27	96.4	314	4	US-09-919-497-82		Sequence 82, Appli
5	27	96.4	356	4	US-09-543-682A-8157		Sequence 8157, Ap
6	27	96.4	587	4	US-09-147-923-2		Sequence 2, Appli
7	27	96.4	597	4	US-09-252-991A-311342		Sequence 311342, A
8	26	92.9	80	3	US-0-247-155-93		Sequence 93, Appli
9	26	92.9	104	4	US-09-210-767-47871		Sequence 47871, A
10	26	92.9	130	4	US-09-107-532A-6103		Sequence 6103, Ap
11	26	92.9	260	4	US-09-439-032A-12019		Sequence 12019, A
12	26	92.9	313	4	US-09-710-271-1758		Sequence 1758, Ap
13	26	92.9	318	1	US-08-220-958-4		Sequence 4, Appli
14	26	92.9	328	3	US-09-134-001C-3229		Sequence 3229, Ap
15	26	92.9	352	4	US-09-19-252-991A-19898		Sequence 19898, A
16	26	92.9	380	3	US-09-316-080-2		Sequence 2, Appli
17	26	92.9	381	4	US-09-489-032A-8085		Sequence 8085, Ap
18	26	92.9	496	4	US-18-622-191-1		Sequence 1, Appli
19	26	92.9	516	3	US-08-888-949-17		Sequence 17, Appli
20	26	92.9	516	3	US-08-888-950-17		Sequence 17, Appli
21	26	92.9	516	3	US-09-262-758-17		Sequence 17, Appli
22	26	92.9	516	4	US-09-885-876-17		Sequence 17, Appli
23	26	92.9	516	4	US-09-895-901-17		Sequence 17, Appli
24	26	92.9	516	4	US-09-731-391-17		Sequence 17, Appli
25	26	92.9	526	4	US-09-910-178B-9		Sequence 9, Appli
26	26	92.9	526	4	US-09-620-461-9		Sequence 9, Appli
27	26	92.9	529	1	US-08-484-815-12		Sequence 31, Appli

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; APPLICATION NUMBER: US 07/778,232
; FILING DATE: 18-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,216
; FILING DATE: 05-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REFERENCE DOCKET NUMBER: 31,215
; TELECOMMUNICATION INFORMATION: WST21BUSA
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-413-805-2

Query Match 96.4%; Score 27; DB 4; Length 265;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 0; Gaps 0;
Qy 1 DEXGLF 6
Db 100 DESGLP 105

RESULT 3
US-09-107-532A-4196
; Sequence 4196, Application US/09107532A
; PATENT NO. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO
; NUMBER OF SEQUENCES: 731.0
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02454
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM 1809660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 30-Jun-1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/1997
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniailo, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; INFORMATION FOR SEQ ID NO: 4196:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:

; ORGANISM: Enterococcus faecium
; FEATURE: misc feature
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...297
; SEQUENCE DESCRIPTION: SEQ ID NO: 4196:
; US-09-107-532A-4196

Query Match 96.4%; Score 27; DB 4; Length 297;
Best Local Similarity 83.3%; Pred. No. 46;
Matches 5; Conservative 0; Gaps 0;
Qy 1 DEXGLF 6
Db 62 DESGLF 67

RESULT 4
US-09-919-497-82
; Sequence 82, Application US/09919497
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; PATENT NO. 6773883
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/725
; CURRENT APPLICATION NUMBER: US/09/919,497
; PRIORITY APPLICATION NUMBER: US 60/221,735
; CURRENT FILING DATE: 2001-07-31
; PRIORITY FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO: 92
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-919-497-82

Query Match 96.4%; Score 27; DB 4; Length 314;
Best Local Similarity 83.3%; Pred. No. 49;
Matches 5; Conservative 0; Gaps 0;
Qy 1 DEXGLF 6
Db 100 DESGLF 105

RESULT 5
US-09-543-681A-8157
; Sequence 8157, Application US/09543681A
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709_1002/001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIORITY APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 6344
; SEQ ID NO: 8157
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-09-543-681A-8157

Query Match 96.4%; Score 27; DB 4; Length 356;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 0; Gaps 0;
Qy 1 DEXGLF 6
Db 132 DESGLF 137

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RESULT 6
US-09-147-923-2
; Sequence 2, Application US/09147923
; Patent No. 6146863
; GENERAL INFORMATION:
;   APPLICANT: Palmer, Leslie M.
;   APPLICANT: Pratt, Julie M.
;   APPLICANT: Hodgson, John E.
;   APPLICANT: Beattie, David T.
;   APPLICANT: Lowe, Adrian M.
;   APPLICANT: Lonetto, Michael A.
;   APPLICANT: Nicholas, Richard O.
;   APPLICANT: Derelewicz, Robert L.
; TITLE OF INVENTION: hcd
; FILE REFERENCE: GM10104
; CURRENT APPLICATION NUMBER: US/09/147,923
; CURRENT FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: 60/060,983
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; LENGTH: 587
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-147-923-2

Query Match Similarity 96.4%; Score 27; DB 3; Length 587;
Best Local Similarity 83.3%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DEXGLF 6
Db 334 DEAGLF 339

RESULT 7
US-09-252-991A-31342
; Sequence 31342, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;   APPLICANT: Marc J. Rubenstein et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 31342
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31342

Query Match Similarity 96.4%; Score 27; DB 4; Length 597;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DEXGLF 6
Db 363 DEAGLF 368

RESULT 8
US-09-247-155-93
; Sequence 93, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:

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STREET: 100 Beaver Street  
 CITY: Waltham  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02454  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD/ROM ISO9660  
 COMPUTER: PC  
 OPERATING SYSTEM: <Unknown>  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/107,532A  
 FILING DATE: 30-Jun-1998  
 PRIORITY NUMBER: 60/085,598  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Aringillo, Pamela Deneke  
 REGISTRATION NUMBER: 40,489  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781) 892-5007  
 TELEFAX: (781) 893-3277  
 INFORMATION FOR SEQ ID NO: 6103:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 130 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: Protein  
 HYPOTHETICAL: YES  
 ORIGINAL SOURCE:  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (B) LOCATION 1..130  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6103:  
 US-09-107-532A-6103

RESULT 11  
 US-09-489-039A-12019  
 Sequence 12019 Application US/09489039A  
 Patent No. 6610836  
 GENERAL INFORMATION:  
 APPLICANT: Gary Breton et. al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 TITLE OF INVENTION: PNEUMONIA FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 2709 2004001  
 CURRENT APPLICATION NUMBER: US/09/489,039A  
 CURRENT FILING DATE: 2000-01-27  
 PRIOR APPLICATION NUMBER: US 60/117,747  
 PRIOR FILING DATE: 1999-01-29  
 NUMBER OF SEQ ID NOS: 14342  
 SEQ ID NO: 12019  
 LENGTH: 260  
 TYPE: PRT  
 ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-12019

Query Match 92.9%; Score 26; DB 4; Length 260;  
 Best Local Similarity 83.3%; Pred. No. 71;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 12  
 US-09-710-279-1758  
 Sequence 1758 Application US/09710279  
 Patent No. 6703492  
 GENERAL INFORMATION:  
 APPLICANT: KIMMELRY, WILLIAM JOHN  
 TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
 FILE REFERENCE: P03480015  
 CURRENT APPLICATION NUMBER: US/09/710,279  
 CURRENT FILING DATE: 2000-11-09  
 PRIORITY NUMBER: 60/164,258  
 PRIOR FILING DATE: 1999-11-09  
 NUMBER OF SEQ ID NOS: 4472  
 SOFTWARE: Patent in Ver. 2.1  
 SEQ ID NO: 1758  
 LENGTH: 313  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: synthetic  
 US-09-710-279-1758

Query Match 92.9%; Score 26; DB 4; Length 313;  
 Best Local Similarity 83.3%; Pred. No. 88;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 13  
 US-08-220-958-4  
 Sequence 4 Application US/08220958  
 Patent No. 5459072  
 GENERAL INFORMATION:  
 APPLICANT: MCKAY, Larry  
 APPLICANT: POLZIN, Kayla  
 TITLE OF INVENTION: FOOD-GRADE INTEGRATION VECTORS FOR  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 STREET: 3100 No. 5459072west Center  
 CITY: Minneapolis  
 STATE: MN  
 COUNTRY: USA  
 ZIP: 55402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/220,958  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION NUMBER:  
 APPLICATION NUMBER: US 07/841,642  
 FILING DATE: 25 FEB 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kowalczyk, Alan W.  
 REGISTRATION NUMBER: 31,535  
 REFERENCE/DOCKET NUMBER: 600-229-US-01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 612-332-5300  
 TELEFAX: 612-332-9081

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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Lactococcus lactis subsp lactis bv.
STRAIN: DRC3
IMMEDIATE SOURCE:
CLONE:
US-08-220-958-4

Query Match 92.9%; Score 26; DB 1; Length 318;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DEXGLF 6
Db 50 DELGLF 55

RESULT 14
US-09-134-001C-3229
Sequence 3229, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134-001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3229
LENGTH: 328
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3229

Query Match 92.9%; Score 26; DB 3; Length 328;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 DEXGLF 6
Db 82 DELGLF 87

RESULT 15
US-09-252-991A-19989
Sequence 19989, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19989
LENGTH: 352

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Title: US-09-699-224A-8

Perfect score: 28

Sequence: 1 DEGLF 6

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 Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	96.4	13	14	US-10-325-694-60
2	27	96.4	13	14	US-10-325-694-61
3	27	96.4	13	14	US-10-325-694-62
4	27	96.4	13	14	US-10-325-694-63
5	27	96.4	123	14	US-10-325-761-10753
6	27	96.4	132	16	US-10-325-761-62289
7	27	96.4	193	14	US-10-325-761-6716
8	27	96.4	244	15	US-10-325-760A-1594
9	27	96.4	244	15	US-10-325-760B-1640
10	27	96.4	265	14	US-10-325-763A-2
11	27	96.4	265	14	US-10-325-724-58
12	27	96.4	275	15	US-10-325-722A-76844
13	27	96.4	310	15	US-10-325-780A-1593

RESULT 1  
 US-10-325-694-60  
 ; Sequence 60, Application US-10325694  
 ; Publication No. US20030148463A1

GENERAL INFORMATION:  
 ; APPLICANT: KUFER, PETER  
 ; APPLICANT: RAUM, TOBIAS  
 ; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN  
 ; TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
 ; FILE REFERENCE: 18164000  
 ; CURRENT APPLICATION NUMBER: US-10-325-694  
 ; CURRENT FILING DATE: 2002-12-19  
 ; PRIOR APPLICATION NUMBER: US-09-403-107  
 ; PRIOR FILING DATE: 1999-10-14  
 ; NUMBER OF SEQ ID NOS: 152  
 ; SEQ ID NO: 60  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC

RESULT 2  
 US-10-325-694-61  
 ; Sequence 61, Application US-10325694  
 ; Publication No. US20030148463A1

US-10-325-694-61  
 ; Sequence 61, Application US-10325694

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Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 61
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-10-325-694-61

Query Match 96.4%; Score 27; DB 14; Length 13;
Best Local Similarity 83.3%; Pred. No. 11; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 5
US-10-156-761-10753
; Sequence 10753, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHITAKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO: 10753
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10753

Query Match 96.4%; Score 27; DB 14; Length 123;
Best Local Similarity 83.3%; Pred. No. 12e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
US-10-767-701-62789
; Sequence 62789, Application US/10767701
; Publication No. US20040172688A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21-53535
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128

Query Match 96.4%; Score 27; DB 14; Length 13;
Best Local Similarity 83.3%; Pred. No. 11; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 4
US-10-325-694-63
; Sequence 63, Application US/10325694
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; FILE REFERENCE: 38164000

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SEQ ID NO 62789  
 LENGTH: 132  
 TYPE: PRT  
 ORGANISM: Sorghum bicolor  
 FEATURE:  
 OTHER INFORMATION: Clone ID: 18065567.pep  
 US-10-767-701-62789

Query Match 96.4%; Score 27; DB 16; Length 132;  
 Best Local Similarity 83.3%; Pred. No. 1.3e+02; Length 132;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEXGLF 6  
 Db 119 DSAGLF 124

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RESULT 7  
 US-10-698-6736  
 Sequence 6736, Application US/10106698  
 Publication No. US2013010969041  
 GENERAL INFORMATION:  
 APPLICANT: Ruben et al.  
 TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide  
 FILE REFERENCE: PA005P1  
 CURRENT APPLICATION NUMBER: US/10/106.698  
 CURRENT FILING DATE: 2002-03-27  
 PRIOR APPLICATION NUMBER: PCT/US00/26524  
 PRIOR FILING DATE: 2000-09-28  
 PRIOR APPLICATION NUMBER: US 60/157,137  
 PRIOR FILING DATE: 1999-09-29  
 PRIOR APPLICATION NUMBER: US 60/163,280  
 PRIOR FILING DATE: 1999-11-03  
 NUMBER OF SEQ ID NOS: 8564  
 SOFTWARE: PatentIn Ver. 3.0  
 SEQ ID NO 736  
 LENGTH: 193  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: MISC\_FEATURE  
 LOCATION: (1)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: MISC\_FEATURE  
 LOCATION: (3)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: MISC\_FEATURE  
 LOCATION: (21)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: MISC\_FEATURE  
 LOCATION: (22)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 NAME/KEY: MISC\_FEATURE  
 LOCATION: (189)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 US-10-698-6736

Query Match 96.4%; Score 27; DB 14; Length 193;  
 Best Local Similarity 83.3%; Pred. No. 1.9e+02; Length 193;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEXGLF 6  
 Db 88 DSAGLF 93

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RESULT 8  
 US-10-374-780A-1594  
 Sequence 1594, Application US/10374780A  
 GENERAL INFORMATION:  
 APPLICANT: Sherman, Bradley K  
 APPLICANT: Riechmann, Jose Luis

RESULT 9  
 US-10-412-699B-1640  
 Sequence 1640, Application US/10412699B  
 Publication No. US2004004509A1  
 GENERAL INFORMATION:  
 APPLICANT: Mendel Biotechnology, Inc.  
 APPLICANT: Zhang, James S.  
 APPLICANT: Fromm, Michael E.  
 APPLICANT: Heard, Jacqueline E.  
 APPLICANT: Riechmann, Jose Luis  
 APPLICANT: Adam, Luc J.  
 APPLICANT: Broun, Pierre E.  
 APPLICANT: Pineda, Omaira  
 APPLICANT: Reuber, T. Lynne  
 APPLICANT: Keddie, James S.  
 APPLICANT: Yu, Guo-Liang  
 APPLICANT: Jiang, Cai-Zhong  
 APPLICANT: Samaha, Raymond R.  
 APPLICANT: Pilgrim, Marsha L.  
 APPLICANT:

APPLICANT: Creelman, Robert A.  
 APPLICANT: Dubell, Arnold N.  
 APPLICANT: Ratcliffe, Oliver  
 APPLICANT: Kumimoto, Roderick K.  
 APPLICANT: Sherman, Bradley K.  
 TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants  
 FILE REFERENCE: MBL-008BCIP  
 CURRENT APPLICATION NUMBER: US/10/412,698B  
 CURRENT FILING DATE: 2003-04-10  
 PRIOR APPLICATION NUMBER: 09/394,519  
 PRIOR FILING DATE: 1999-09-13  
 PRIOR APPLICATION NUMBER: 09/489,376  
 PRIOR FILING DATE: 2000-01-21  
 PRIOR APPLICATION NUMBER: 09/506,720  
 PRIOR FILING DATE: 2000-02-17  
 PRIOR APPLICATION NUMBER: 09/533,030  
 PRIOR FILING DATE: 2000-03-22  
 PRIOR APPLICATION NUMBER: 09/533,392  
 PRIOR FILING DATE: 2000-03-22  
 PRIOR APPLICATION NUMBER: 09/533,029  
 PRIOR FILING DATE: 2000-03-22  
 PRIOR APPLICATION NUMBER: 09/532,591  
 PRIOR FILING DATE: 2000-03-22  
 PRIOR APPLICATION NUMBER: 09/533,648  
 PRIOR FILING DATE: 2000-03-22  
 PRIOR APPLICATION NUMBER: 09/713,994  
 PRIOR FILING DATE: 2000-11-16  
 PRIOR FILING NUMBER: 09/819,142  
 PRIOR FILING DATE: 2001-03-27  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 2011  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 1660  
 LENGTH: 244  
 TYPE: PRT  
 ORGANISM: Oryza sativa  
 US-10-412,698B-1640

Query Match 96.4%; Score 27; DB 15; Length 244;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEXGLF 6  
 Db 26 DEAGLF 31

RESULT 10  
 US-10-299-383-2  
 / Sequence 2, Application US/10299383  
 / Publication No. US20030103935A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Linnenbach, Alban J.  
 / Koprkowski, Hilary  
 / Heslyn, Dorothy  
 / TITLE OF INVENTION: Soluble Variants of Type I Membrane  
 / NUMBER OF SEQUENCES: 4  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Howson and Howson  
 / STREET: P.O. Box 457 Spring House Corporate Center  
 / CITY: Spring House  
 / STATE: Pennsylvania  
 / COUNTRY: USA  
 / ZIP: 19477  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0  
 / CURRENT APPLICATION NUMBER: US/10/299,383  
 / APPLICATION NUMBER: US20030103935A1-2002  
 / FILING DATE: 19-No. US20030103935A1-2002

/ APPLICANT: Zyskind, Judith  
 / APPLICANT: Wall, Daniel  
 / APPLICANT: Trawick, John  
 / APPLICANT: Carr, Grant  
 / APPLICANT: Yamamoto, Robert  
 / APPLICANT: Forbush, R.  
 / APPLICANT: Xu, H.  
 / TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 / FILE REFERENCE: ELTRA-034A  
 / CURRENT APPLICATION NUMBER: US/10/282,122A  
 / CURRENT FILING DATE: 2003-02-20  
 / PRIOR APPLICATION NUMBER: 60/191,078  
 / PRIOR FILING DATE: 2000-03-21  
 / PRIOR APPLICATION NUMBER: 60/206,848  
 / PRIOR FILING DATE: 2000-05-23  
 / PRIOR APPLICATION NUMBER: 60/207,727  
 / PRIOR FILING DATE: 2000-05-26  
 / PRIOR APPLICATION NUMBER: 60/230,335  
 / PRIOR FILING DATE: 2000-09-06  
 / PRIOR APPLICATION NUMBER: 60/230,347  
 / PRIOR FILING DATE: 2000-09-09  
 / PRIOR APPLICATION NUMBER: 60/242,578  
 / PRIOR FILING DATE: 2000-10-23  
 / PRIOR APPLICATION NUMBER: 60/253,625  
 / PRIOR FILING DATE: 2000-11-27  
 / PRIOR APPLICATION NUMBER: 60/257,931  
 / PRIOR FILING DATE: 2000-12-22  
 / PRIOR APPLICATION NUMBER: 60/267,636  
 / PRIOR FILING DATE: 2001-02-09  
 / PRIOR APPLICATION NUMBER: 60/269,308  
 / PRIOR FILING DATE: 2001-02-16  
 / Remaining Prior Application data removed - See File Wrapper or P.M.  
 / NUMBER OF SEQ ID NOS: 78614  
 / SOFTWARE: Patentin version 3.1  
 / TYPE: PRT  
 / ORGANISM: Ureaplasma urealyticum  
 US-10-282-122A-76844

Query Match 96.4%; Score 27; DB 15; Length 275;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEYGLF 6  
 Db 231 DETGLF 23 6

RESULT 13  
 US-10-374-780A-1593  
 / Sequence 1593, Application US/10374780A  
 / Publication No. US20040019927A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Sherman, Bradley K  
 / APPLICANT: Riechmann, Jose Luis  
 / APPLICANT: Jiang, Cai-Zhong  
 / APPLICANT: Heard, Jacqueline E  
 / APPLICANT: Haake, Volker  
 / APPLICANT: Creeiman, Robert A  
 / APPLICANT: Ratcliffe, Oliver  
 / APPLICANT: Adam, Luc J  
 / APPLICANT: Reuber, T. Lynne  
 / APPLICANT: Keddie, James E  
 / APPLICANT: Broun, Pierre E  
 / APPLICANT: Pilgrim, Marsha L  
 / APPLICANT: Dubell III, Arnold T  
 / APPLICANT: Pineda, Omaira  
 / APPLICANT: Yu, Guo-Liang  
 / TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants  
 / FILE REFERENCE: NBI-0048CIP  
 / CURRENT APPLICATION NUMBER: US/10/412,699B  
 / CURRENT FILING DATE: 2003-04-10  
 / PRIOR APPLICATION NUMBER: 09/394,519  
 / PRIOR FILING DATE: 1999-09-13  
 / PRIOR APPLICATION NUMBER: 09/489,376  
 / PRIOR FILING DATE: 2000-01-21  
 / PRIOR APPLICATION NUMBER: 09/506,720  
 / PRIOR FILING DATE: 2000-02-17  
 / PRIOR APPLICATION NUMBER: 09/533,030  
 / PRIOR FILING DATE: 2000-03-22

/ TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS  
 / FILE REFERENCE: NBI-0047 CIP  
 / CURRENT APPLICATION NUMBER: US/10/374,780A  
 / CURRENT FILING DATE: 2003-02-25

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; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,648
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/819,142
; PRIOR FILING DATE: 2001-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 1639
; LENGTH: 310
; TYPE: PROT
; ORGANISM: Oryza sativa
US-10-412-699B-1639

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Query Match      96.4%;  Score 27;  DB 15;  Length 310;
Best Local Similarity  83.3%;  Pred. No. 3.1e+02;
Matches 5;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;
Qy  1  DEXGLF 6
    |||||
Db  26  DEAGLF 31

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RESULT 15
US-10-437-963-162911
; Sequence 162911, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;   APPLICANT: La Rosa, Thomas J.
;   APPLICANT: Kovacic, David K.
;   APPLICANT: Zhou, Yihua
;   APPLICANT: Cao, Yongwei
;   APPLICANT: Wu, Wei
;   APPLICANT: Boukharov, Andrey A.
;   APPLICANT: Barbazuk, Brad
;   APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;   TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 162911
; LENGTH: 310
; TYPE: PROT
; ORGANISM: Oryza sativa
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61957C.1.pep
US-10-437-963-162911

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Query Match      96.4%;  Score 27;  DB 16;  Length 310;
Best Local Similarity  83.3%;  Pred. No. 3.1e+02;
Matches 5;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;
Qy  1  DEXGLF 6
    |||||
Db  26  DEAGLF 31

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RESULT 7							
RP	SEQUENCE FROM N.A.						
RC	STRAIN=TH3996;						
RA	MEDLINE=20448934; PubMed=10992480;						
RT	"Genetic characterization of DNA region containing the trn and ure genes of <i>Vibrio parahaemolyticus</i> ,"						
RL	<i>Infect. Immun.</i> 68:5742-5748 (2000).						
[2]	SEQUENCE FROM N.A.						
RP	STRAIN=TH3996;						
RC	Submitted (FEB-2001) to the EMBL/GenBank/DDJB databases.						
RA	EMBL; AB038238; BAB13789_1; -.						
RA	HSSP; P18317; 1GMW.						
DR	GO; GO:0016151; P:nickel ion binding; IEA.						
DR	GO; GO:0006461; P:protein complex assembly; IEA.						
DR	GO; GO:0019627; P:urea metabolism; IEA.						
DR	InterPro; IPR007864; UriE_C.						
DR	InterPro; IPR004029; UriE_N.						
PFam; PF05194; UriE_C; 1.							
PFam; PF02814; UriE_N; 1.							
SEQUENCE	159 AA; 17592 MW; 362146808B5440F7 CRC64;						
Qy	1 DEXGLF 6						
Db	4 DEAGLFP 50						
RESULT 6							
Q8G1K1	Q8G1K1 PRELIMINARY; PRT; 231 AA.						
ID	08G1K1						
AC	Q8G1K1;						
DT	01-MAR-2003 (TREMBLrel. 23; Created)						
DT	01-MAR-2003 (TREMBLrel. 23; Last sequence update)						
DT	01-MAR-2003 (TREMBLrel. 23; Last annotation update)						
DE	Hypothetical protein.						
GN	OrderedLocusNames=BR0714;						
BR0714	Brucella suis.						
OC	Bacteria; Alphaproteobacteria; Rhizobiales;						
OC	Brucellales; Brucellaceae.						
NCBI_TaxID=29461;							
[1]	SEQUENCE FROM N.A.						
RA	STRAIN=1330 / Biora 1;						
RA	MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.1923190929;						
RA	Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A., Van Aken S.E., Riedmiller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Hailing S.M., Boyle S.M., Fraser C.M., "The <i>Brucella suis</i> genome reveals fundamental similarities between animal and plant pathogens and symbionts,"						
RA	<i>Proc. Natl. Acad. Sci. U.S.A.</i> 99:13148-13153 (2002).						
RA	TIGR; BR0714; -.						
DR	DR04377; AN29643_1; -.						
CC	Complete proteome; Hypothetical protein.						
SEQUENCE	231 AA; 25232 MW; B2101DBBA1752831 CRC64;						
Qy	1 DEXGLF 6						
Db	4 DEAGLFP 50						
RESULT 8							
Q8G1K1	Q8G1K1 STANDARD; PRT; 259 AA.						
ID	UPK3_BACCI						
AC	P62463; BACCI						
DT	05-JUL-2004 (Rel. 44, Created)						
DT	05-JUL-2004 (Rel. 44, Last sequence update)						
DE	Putative undecaprenol kinase 3 (EC 2.7.1.66) (Bacitracin resistance protein 3).						
DB	Name=upk3; Synonyms=baci3; OrderedLocusName=BCE2732;						
GN	Bacillus cereus (strain ATCC 10989).						
OS	Bacteria; Firmicutes; Bacillales;						
OC	NCBI_TaxID=2252523;						
RN	SEQUENCE FROM N.A.						
RA	STRAIN=1330 / Biora 1;						
RA	MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.1923190929;						
RA	Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A., Van Aken S.E., Riedmiller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Hailing S.M., Boyle S.M., Fraser C.M., "The <i>Brucella suis</i> genome reveals fundamental similarities between animal and plant pathogens and symbionts,"						
RA	<i>Proc. Natl. Acad. Sci. U.S.A.</i> 99:13148-13153 (2002).						
RA	TIGR; BR0714; -.						
DR	DR04377; AN29643_1; -.						
CC	Complete proteome; Hypothetical protein.						
SEQUENCE	231 AA; 25232 MW; B2101DBBA1752831 CRC64;						
Qy	1 DEXGLF 6						
Db	4 DEAGLFP 50						
RESULT 9							
Q8G1K1	Q8G1K1 PRELIMINARY; PRT; 231 AA.						
ID	08G1K1						
AC	Q8G1K1;						
DT	01-MAR-2003 (TREMBLrel. 23; Created)						
DT	01-MAR-2003 (TREMBLrel. 23; Last sequence update)						
DT	01-MAR-2003 (TREMBLrel. 23; Last annotation update)						
DE	Hypothetical protein.						
GN	OrderedLocusNames=BR0714;						
BR0714	Brucella suis.						
OC	Bacteria; Alphaproteobacteria; Rhizobiales;						
OC	Brucellales; Brucellaceae.						
NCBI_TaxID=29461;							
[1]	SEQUENCE FROM N.A.						
RA	STRAIN=1330 / Biora 1;						
RA	MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.1923190929;						
RA	Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A., Van Aken S.E., Riedmiller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Hailing S.M., Boyle S.M., Fraser C.M., "The <i>Brucella suis</i> genome reveals fundamental similarities between animal and plant pathogens and symbionts,"						
RA	<i>Proc. Natl. Acad. Sci. U.S.A.</i> 99:13148-13153 (2002).						
RA	TIGR; BR0714; -.						
DR	DR04377; AN29643_1; -.						
CC	Complete proteome; Hypothetical protein.						
SEQUENCE	231 AA; 25232 MW; B2101DBBA1752831 CRC64;						
Qy	1 DEXGLF 6						
Db	4 DEAGLFP 50						
RESULT 10							
Q8G1K1	Q8G1K1 PRELIMINARY; PRT; 231 AA.						
ID	08G1K1						
AC	Q8G1K1;						
DT	01-MAR-2002 (TREMBLrel. 20; Created)						
DT	01-MAR-2002 (TREMBLrel. 20; Last sequence update)						
DT	01-JUN-2003 (TREMBLrel. 24; Last annotation update)						
DE	INSERTION SEQUENCE						
GN	SEQUENCEFROMN.A.; BMEI1238;						
OS	Brucella melitensis.						
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;						
OC	Brucellales; Brucellaceae.						
NCBI_TaxID=29461;							
[1]	SEQUENCE FROM N.A.						
RA	STRAIN=1330 / Biora 1;						
RA	MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.1923190929;						
RA	Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A., Van Aken S.E., Riedmiller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Hailing S.M., Boyle S.M., Fraser C.M., "The <i>Brucella suis</i> genome reveals fundamental similarities between animal and plant pathogens and symbionts,"						
RA	<i>Proc. Natl. Acad. Sci. U.S.A.</i> 99:13148-13153 (2002).						
RA	TIGR; BR0714; -.						
DR	DR04377; AN29643_1; -.						
CC	Complete proteome; Hypothetical protein.						
SEQUENCE	231 AA; 25232 MW; B2101DBBA1752831 CRC64;						
Qy	1 DEXGLF 6						
Db	4 DEAGLFP 50						

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DR EMBL; AE017272; AAS1644.1; -.

DR HAMAP; MF\_01006; -; 1.

DR InterPro; IPR003824; BacA.

DR Pfam; PF02673; BacA; 1.

KW Antibiotic resistance; Complete proteome; Kinase; Transferase;

KW Transmembrane.

FT TRANSMEM 7 29 Potential.

FT TRANSMEM 39 58 Potential.

FT TRANSMEM 70 92 Potential.

FT TRANSMEM 102 120 Potential.

FT TRANSMEM 172 194 Potential.

FT TRANSMEM 209 231 Potential.

FT TRANSMEM 238 255 Potential.

SEQUENCE 259 AA; 29186 MW; 24435D0APR4CB8D3C CRC64;

Qy 1 DEXGLP 6

Db 37 DEAGLP 42

RESULT 10

Q6H121 PRELIMINARY; PRT; 259 AA.

ID Q6H121; 05-JUL-2004 (TREMBLrel. 27, Created)

AC Q6H121; 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Probable undecaprenol kinase (Bacitracin resistance protein) (EC

Name=bACa; ORFNames=BT9727\_2479;

OS Bacillus thuringiensis serovar konkukian str. 97-27.

RA Bretton T.S., Bruce D., Challacombe J.P., Gilna P., Han C., Hill K.,

RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,

RA Richardson P., Rubin E., Tice H.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE017355; AA16038.1; -.

DR InterPro; IPR03824; BacA.

DR Pfam; PF02673; BacA; 1.

KW Kinase; Transferase.

SEQUENCE 259 AA; 29058 MW; 36101D761CD9EA8E CRC64;

Qy 1 DEXGLP 6

Db 37 DEAGLP 42

RESULT 11

AAS1644 PRELIMINARY; PRT; 259 AA.

ID AAS1644; 02-MAR-2004 (TREMBLrel. 27, Created)

AC AAS1644; 02-MAR-2004 (TREMBLrel. 27, Last sequence update)

DT 04-MAY-2004 (TREMBLrel. 27, Last annotation update)

DE Undecaprenol kinase, putative (EC 2.7.1.66).

GN Bacillus cereus (strain ATCC10887).

RA Bacterium; Firmicutes; Bacillales; Bacillaceae; Bacillus.

RA Overbeek R., Kyrpides N.C.;

RA "Genome sequence of *Bacillus cereus* and comparative analysis with

RT *Bacillus anthracis*.";

RT MEDLINE:22608415; PubMed:12721630; DOI:10.1038/nature01582;

RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelier B.,

RA Kapral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,

RA Chu L., Mazur M., Gotsman E., Larsen N., Walunas T.,

RA Greshkin Y., Pusch G., Habelkorn R., Fonstein M., Ehrlich S.D.,

RA Overbeek R., Kyrpides N.C.;

RA "Genome sequence of *Bacillus cereus* and comparative analysis with

RT *Bacillus anthracis*.";

RT FUNCTION: Probably phosphorylates undecaprenol to undecaprenyl

phosphate. Confers resistance to bacitracin (By similarity).

CC CATALYTIC ACTIVITY: ATP + undecaprenol = ADP + undecaprenyl

phosphate.

CC SUBCELLULAR LOCATION: Integral membrane protein (Probable).

CC -I- MISCELLANEOUS: Bacitracin is thought to be involved in inhibition

CC of peptidoglycan synthesis by sequestering undecaprenyl

CC diphosphate reducing the pool of lipid carrier available.

CC -I- SIMILARITY: Belongs to the upk family.

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CC or send an email to license@isb-sib.ch).

EMBL; AE017006; AAP09665.1; -.

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CC DR EMBL; AE017272; AAS1644.1; -.

CC DR HAMAP; MF\_01006; -; 1.

CC DR InterPro; IPR003824; BacA.

CC DR Pfam; PF02673; BacA; 1.

CC KW Antibiotic resistance; Complete proteome; Kinase; Transferase;

CC KW Transmembrane.

CC FT TRANSMEM 7 29 Potential.

CC FT TRANSMEM 39 58 Potential.

CC FT TRANSMEM 70 92 Potential.

CC FT TRANSMEM 102 119 Potential.

CC FT TRANSMEM 140 162 Potential.

CC FT TRANSMEM 172 194 Potential.

CC FT TRANSMEM 206 228 Potential.

CC FT TRANSMEM 238 255 Potential.

CC SQ SEQUENCE 259 AA; 29209 MW; 545969859BB8A16 CRC64;

CC Qy 1 DEXGLP 6

CC Db 37 DEAGLP 42

CC RESULT 10

CC Q6H121 PRELIMINARY; PRT; 259 AA.

CC ID Q6H121; 05-JUL-2004 (TREMBLrel. 27, Created)

CC AC Q6H121; 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

CC DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

CC DE Probable undecaprenol kinase (Bacitracin resistance protein) (EC

CC Name=bACa; ORFNames=BT9727\_2479;

CC OS Bacillus thuringiensis serovar konkukian str. 97-27.

CC RA Bretton T.S., Bruce D., Challacombe J.P., Gilna P., Han C., Hill K.,

CC RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,

CC RA Richardson P., Rubin E., Tice H.;

CC RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

CC DR EMBL; AE017355; AA16038.1; -.

CC DR InterPro; IPR03824; BacA.

CC DR Pfam; PF02673; BacA; 1.

CC KW Kinase; Transferase.

CC SEQUENCE 259 AA; 29058 MW; 36101D761CD9EA8E CRC64;

CC Qy 1 DEXGLP 6

CC Db 37 DEAGLP 42

CC RESULT 11

CC AAS1644 PRELIMINARY; PRT; 259 AA.

CC ID AAS1644; 02-MAR-2004 (TREMBLrel. 27, Created)

CC AC AAS1644; 02-MAR-2004 (TREMBLrel. 27, Last sequence update)

CC DT 04-MAY-2004 (TREMBLrel. 27, Last annotation update)

CC DE Undecaprenol kinase, putative (EC 2.7.1.66).

CC GN Bacillus cereus (strain ATCC10887).

CC RA Bacterium; Firmicutes; Bacillales; Bacillaceae; Bacillus.

CC Overbeek R., Kyrpides N.C.;

CC "Genome sequence of *Bacillus cereus* and comparative analysis with

CC *Bacillus anthracis*.";

CC MEDLINE:22608415; PubMed:12721630; DOI:10.1038/nature01582;

CC RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelier B.,

CC RA Kapral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,

CC RA Chu L., Mazur M., Gotsman E., Larsen N., Walunas T.,

CC RA Greshkin Y., Pusch G., Habelkorn R., Fonstein M., Ehrlich S.D.,

CC RA Overbeek R., Kyrpides N.C.;

CC RA "Genome sequence of *Bacillus cereus* and comparative analysis with

CC *Bacillus anthracis*.";

CC FUNCTION: Probably phosphorylates undecaprenol to undecaprenyl

phosphate. Confers resistance to bacitracin (By similarity).

CC CATALYTIC ACTIVITY: ATP + undecaprenol = ADP + undecaprenyl

phosphate.

CC SUBCELLULAR LOCATION: Integral membrane protein (Probable).

CC -I- MISCELLANEOUS: Bacitracin is thought to be involved in inhibition

CC of peptidoglycan synthesis by sequestering undecaprenyl

CC diphosphate reducing the pool of lipid carrier available.

CC -I- SIMILARITY: Belongs to the upk family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the European Bioinformatics Institute and the EMBL outstation -

CC use by non-profit institutions. There are no restrictions on its

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

EMBL; AE017006; AAP09665.1; -.

RX	PubMed=114960714;	KW	Complete proteome; DNA repair; Glycosidase; Hydrolase; Zinc;
RA	Rasko D.A., Ravel J., Osekstad O.A., Helgason E., Cer R.Z., Jiang L.,	KW	Zinc finger.
RA	Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,	FT	250
RA	Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;	SEQUENCE	275 AA; 31993 MW; 9F4624E870E5AF6A CRC64;
RT	"The genome sequence of <i>Bacillus cereus</i> ATCC 10987 reveals metabolic adaptations and a large plasmid related to <i>Bacillus anthracis</i> pXO1."	Query Match	96.4%; Score 27; DB 1; Length 275;
RT	RL	Best Local Similarity	83.3%; Pred. No. 2.5e+02;
RL	EMBL; AE017272; AA541644.1; -.	Matches	0; Mismatches 1; Indels 0; Gaps 0;
DR	TIGR; BCE2732; -.	Qy	1 DBXGLP 6
DR	Kinase; Transferase. 259 AA; 29209 MW; 545969EB59BB8A16 CRC64;	Db	231 DETGLP 236
SEQUENCE	259 AA;	RESULT 13	
Query Match	96.4%; Score 27; DB 2; Length 259;	Y818_PYRAE	PYRAE STANDARD; PRT; 281 AA.
Best Local Similarity	83.3%; Pred. No. 2.3e+02;	ID	Y818_PYRAE
Matches	0; Mismatches 1; Indels 0; Gaps 0;	AC	Q8ZY11;
Qy	1 DEXGLP 6	DT	28-FPB-2003 (Rel. 41, Created)
Db	37 DEAGLF 42	DT	28-FPB-2003 (Rel. 41, Last sequence update)
DEAGLF	42	DT	05-JUL-2004 (Rel. 44, Last annotation update)
RESULT 12		DE	Hypothetical UPF0103 protein PAE0818.
FPG_UREPA	STANDARD;	GN	OrderedLocusNames=PAE0818;
ID	PRT; 275 AA.	OS	Pyrobaculum aerophilum.
FPG_UREPA	STANDARD;	OC	Thermoproteaceae; Pyrobaculum; Thermoproteales;
AC	Q9PQ76;	RA	Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
DT	28-FPB-2003 (Rel. 41, Created)	PA	Pyrobaculum aerophilum.
DT	28-FPB-2003 (Rel. 41, Last sequence update)	RT	"Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
DE	Formamidoimidine-DNA glycosylase (EC 3.2.2.23) (Fapy-DNA	RL	Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
DE	9Glycosylase).	CC	-!- SIMILARITY: Belongs to the UPF0103 Family.
GN	Name=symt; Synonyms=fpg; OrderedLocusNames=U4143;	CC	-----
OS	Ureaplasma parvum (Ureaplasma urealyticum biotype 1).	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
OX	NCBI_TaxID=134821;	CC	the European Bioinformatics Institute. There are no restrictions on its
RN	[1]	CC	use by non-profit institutions as long as its content is in no way
RP	SEQUENCE FROM N.A.	CC	modified and this statement is not removed. Usage by and for commercial
RC	STRAIN=Server 3;	CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
RX	MEDLINE=200500219; PubMed=11048724; DOI=10.1038/35037619;	CC	-----
RA	Glass J.I., Leikowitz B.J., Glass J.S., Heiner C.R., Chen E.Y.,	CC	-----
RA	Cassell G.H.;	CC	-----
RT	"The complete sequence of the mucosal pathogen Ureaplasma urealyticum."	CC	-----
RT	Nature 407:757-762 (2000).	CC	-----
RL	-!- FUNCTION: This enzyme may play a significant role in processes leading to recovery from mitogenesis and/or cell death by alkylating agents (By similarity).	CC	-----
CC	-!- CATALYTIC ACTIVITY: Hydrolysis of DNA containing ring-opened N(7) -	CC	-----
CC	methylguanine residues, releasing 2,6-diamino-4-hydroxy-5-(N-methyl)formamidopyrimidine.	CC	-----
CC	-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).	CC	-----
CC	-!- SIMILARITY: Belongs to the FPG family.	CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -	CC	-----
CC	the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	CC	-----
CC	HSSP; P42371; AAF30824.1; -.	CC	-----
DR	HAMAP; MF_00103; -.	DR	RESULT 14
DR	InterPro; IPR00214; Fapy DNA Zn BS.	Q9ZU57	PRELIMINARY; PRT; 283 AA.
DR	InterPro; IPR000191; Fapy DNA glyco.	ID	Q9ZU57;
DR	InterPro; IPR010979; Ribosomal H2TH.	AC	Q9ZU57; (T-EMBLrel. 10, Created)
DR	InterPro; IPR010663; ZF-Finger.	DT	01-MAY-1999 (T-EMBLrel. 10, Last annotation update)
DR	Pfam; PF01149; Fapy DNA glyco; 1.	PFAM	01-MAY-1999 (T-EMBLrel. 10, Last annotation update)
DR	Pfam; PF06633; H2TH; 1.	DR	01-MAR-2004 (T-EMBLrel. 10, Last annotation update)
DR	ProDom; PDD03680; Fapy DNA glyco; 1.	DR	Putative CENP-B/ARS binding protein-like protein.
DR	TIGRFAMs; TIGR05577; Fpg; 1.	DR	Name=At2g06660;
DR	PROSITE; PS01242; Fpg; 1.	GN	

OS Arabidopsis thaliana (Mouse-ear cress). Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euroids II; Brassicales; Brassicaceae; Arabidopsis. [1]

NCBI\_TaxID=3702;

RN [1]

SEQUENCE FROM N.A.

RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E., Barnstead M.E., Mason T.M., Bowman C.J., Bonning C.M., Benito M.-I., Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C., Fraser C.M., Venter J.C., Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RA [2]

RN SEQUENCE FROM N.A.

RA Town C.D., Kaul S.; Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC006165; AD14510.1; -.

DR PIR; B84479; B84479.

DR GO; GO:0005634; C-nucleus; IEA.

DR GO; GO:0003676; F-nucleic acid binding; IEA.

DR InterPro; IPR004875; CENP-B.

DR InterPro; IPR009077; Homeodomain-like.

DR Pfam; PF03184; DDE; 1.

SEQUENCE 283 AA; 33068 MW; 8401D57F17BA63C4 CRC64;

Qy 1 DEXGLP 6

Db 81 DEXGLP 86

RESULT 15

Q94D31 PRELIMINARY; PRT; 310 AA.

AC Q94D31;

DT 01-DEC-2001 (TREMBrel. 19, Created)

DT 01-OCT-2004 (TREMBrel. 28, Last sequence update)

DE P012E02.25 protein (WRKY transcription factor 27) (P0700A11.6

GN Name=P012E02.25; Synonyms=P0700A11.6, WRKY27;

OS Oryza sativa (japonica cultivar-group).

OC Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Embryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartideae; Oryzeae; Oryza.

NCBI\_TaxID=39947;

RN [1]

SEQUENCE FROM N.A.

RA Sasaki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Hosokawa S., Masukawa M., Arikawa K., Chidén Y., Hayashi M., Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M., Ikeno M., Ichō S., Itōh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K., Karasawa K., Katagiri S., Kobayashi N., Kono I., Machida K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y., Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M., Shimokawa T., Shomura A., Song J., Takasaki Y., Terasawa K., Tsuji K., Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Zhang H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Sun M.Y., Yano M., Jiang J., Gotohori T.,

RT "The genome sequence and structure of rice chromosome 1.";

RT Nature 420:312-316 (2002).

RN [2]

SEQUENCE FROM N.A.

RP PubMed-15047897.

RA Zhang Z.-L., Xie Z., Zou X., Casaretto J., Ho T.H., Shen Q.J.;

RT "A rice WRKY gene encodes a transcriptional repressor of the gibberellin signaling pathway in aleurone cells.";

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	30	26	92.9	345	2	C84489
OM protein - protein search, using sw model		31	26	92.9	375	2	A87665
Run on:	January 3, 2005, 13:43:11 ; Search time 38 Seconds	32	26	92.9	381	2	B69722
Title:	US-09-699-224A-8	33	26	92.9	383	1	S15624
Perfect Score:	28	34	26	92.9	385	2	T03003
Sequence:	1 DEXGLF 6	35	26	92.9	390	2	T44324
Scoring table:	BLOSUM62	36	26	92.9	417	2	JCS326
Scoring table:	BLOSUM62	37	26	92.9	496	2	S71205
Scoring table:	BLOSUM62	38	26	92.9	526	2	S70587
Scoring table:	BLOSUM62	39	26	92.9	526	2	A37821
Scoring table:	BLOSUM62	40	26	92.9	646	2	S01352
Scoring table:	BLOSUM62	41	26	92.9	809	2	T18970
Scoring table:	BLOSUM62	42	26	92.9	810	2	T19879
Scoring table:	BLOSUM62	43	26	92.9	811	2	S17908
Scoring table:	BLOSUM62	44	26	92.9	831	2	S62751
Scoring table:	BLOSUM62	45	26	92.9	1417	2	H90670
Searched:	283416 seqs, 96216763 residues						ALIGNMENTS
Total number of hits satisfying chosen parameters:	283416						
Minimum DB seq length: 0							RESULT 1
Maximum DB seq length: 2000000000							F69026
Post-processing: Minimum Match 0%							Conserved hypothetical protein MTH1197 - Methanobacterium thermoautotrophicum (strain De)
Post-processing: Maximum Match 100%							C;Species: Methanobacterium thermoautotrophicum
Post-processing: Maximum Match 100%							C;Date: 05-Dec-1997 #text_change 09-Jul-2004
Post-processing: Maximum Match 100%							C;Accession: F69026
Post-processing: Maximum Match 100%							R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I;
Post-processing: Maximum Match 100%							R;Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
Post-processing: Maximum Match 100%							ki, S.; Church, G.M.; Daniels, C.J.; Mac, J.; Rice, P.; Noelling, J.; Reeve, J.N.
Post-processing: Maximum Match 100%							J. Bacteriol. 179, 7135-7155, 1997
Post-processing: Maximum Match 100%							A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
Post-processing: Maximum Match 100%							A;Reference number: A69000; PMID:38037514; PMID:9371463
Post-processing: Maximum Match 100%							A;Accession: F69026
Post-processing: Maximum Match 100%							A;Status: preliminary; nucleic acid sequence not shown; translation not shown
Post-processing: Maximum Match 100%							A;Molecule type: DNA
Post-processing: Maximum Match 100%							A;Residues: 1-146 <MTH>
Post-processing: Maximum Match 100%							A;Cross-references: UNIPROT:O27265; GB:AE000888; PMID:92622304; PIDN: AABB5686
Post-processing: Maximum Match 100%							A;Experimental source: strain Delta H
Post-processing: Maximum Match 100%							C;Genetics:
Post-processing: Maximum Match 100%							A;Gene: MTH1197
Post-processing: Maximum Match 100%							A;Start codon: TTG
Database :	PIR 79;*						
Database :	1: pir1;*						Qy 1 DEXGIP 6
Database :	2: pir2;*						Db 117 DETGIP 122
Database :	3: pir3;*						
Database :	4: pir4;*						
Pred. No. is the number of results predicted by chance to have a							RESULT 2
score greater than or equal to the score of the result being printed,							AH3406
and is derived by analysis of the total score distribution.							Insertion sequence IS21 probable ATP-binding protein BMEII1238 [imported] - Brucella melit
SUMMARIES							C;Species: Brucella melitensis
%							C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
Result No.	Score	Query Match	Length	DB ID	Description		
1	27	96.4	146	2 F69026	conserved hypothetical insertion sequence	Best Local Similarity 83.3%;	Score 27; DB 2; Length 146;
2	27	96.4	231	2 AH3406	formanidopyrimidin	Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Pred. No. 34;
3	27	96.4	275	2 BB8295	hypothetical prote		
4	27	96.4	283	2 BB8479	epithelial glycop		
5	27	96.4	314	2 JCS94	jerky gene protein		
6	27	96.4	442	2 JCS594	flavin containing		
7	27	96.4	469	2 AG3139	JH8 protein - huma		
8	27	96.4	520	2 BZ0225	hypothetical prote		
9	27	96.4	605	2 B398148	hypothetical prote		
10	27	96.4	694	2 B397630	hypothetical prote		
11	27	96.4	694	2 B398153	conserved hypothet		
12	27	96.4	753	2 C89786	hypothetical prote		
13	26	92.9	108	1 PVFG	parvalbumin beta -		
14	26	92.9	111	1 A69332	hypothetical prote		
15	26	92.9	143	2 G71880	hypothetical prote		
16	26	92.9	143	2 F66634	hypothetical prote		
17	26	92.9	161	2 S04765	LAT52 protein prec		
18	26	92.9	174	2 F83581	heme d1 biosynthes		
19	26	92.9	204	2 T47721	hypothetical prote		
20	26	92.9	205	2 G71216	probable S-adenos		
21	26	92.9	212	2 F83917	hypothetical prote		
22	26	92.9	235	2 AD2274	uroporphyrinogen-I		
23	26	92.9	273	2 I39791	transcription-regu		
24	26	92.9	295	2 A64756	attachment and effa		
25	26	92.9	313	2 G81145	hypothetical prote		
26	26	92.9	314	1 A6489	pan-epithelial gly		
27	26	92.9	318	2 A43746	nisin resistance p		
28	26	92.9	322	2 G65946	phage-related prot		
29	26	92.9	337	2 H64389	isocitrate dehydro		

Query Match 96.4%; Score 27; DB 2; Length 231;  
Best Local Similarity 83.3%; Pred. No. 53;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 DEXGLF 6  
Db 102 DETGLF 107

RESULT 3

B82895 formamidopyrimidine-DNA Glycosylase UU413 [Imported] - Ureaplasma urealyticum  
C;Species: Ureaplasma urealyticum  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
C;Accession: B82895  
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
Submitted to GenBank, February 2000  
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a minor  
A;Accession: B82870  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-275 <GLA>  
A;Cross-references: GB:AB002138; GB:AF222894; NID:96899390; PIDN:AAF30824.1; GSPDB:GN001  
A;Experimental source: serovar 3; biovar 1  
C;Generics:  
A;Gene: fpg; UU413  
A;Genetic code: SCG3  
C;Superfamily: formamidopyrimidine-DNA glycosidase

Query Match 96.4%; Score 27; DB 2; Length 275;  
Best Local Similarity 83.3%; Pred. No. 63;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 DEXGLF 6  
Db 231 DETGLF 236

RESULT 4

B84479 hypothetical protein At2g06660 [Imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: B84479  
P;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umavam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ventner, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Accession: A84420; PMID:10617197  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-283 <STO>  
A;Cross-references: UNIPROT:Q9ZU57; GB:AB002093; NID:94262216; PIDN:AA014510.1; GSPDB:GN  
A;Generics:  
A;Gene: At2g06660  
A;Map position: 2

Query Match 96.4%; Score 27; DB 2; Length 283;  
Best Local Similarity 83.3%; Pred. No. 65;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 DEXGLF 6  
Db 81 DETGLF 86

RESULT 5

B48149 epithelial glycoprotein antigen GA733-2 precursor - human  
N;Alternate names: adenocarcinoma-associated glycoprotein gp40; carcinoma-associated and

C;Species: Homo sapiens (man)  
C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: B48149; A35907; IJ5995; A31377; A45898; A0799; A61569; PID:9182906  
R;Linnemann, B.J.; Seng, B.A.; Wu, S.; Robbins, S.; Scollon, M.; Pyrc, J.J.; Druck, T.;  
Mol. Cell. Biol. 13, 1507-1515, 1993  
A;Title: Retroposition in a family of carcinoma-associated antigen genes.  
A;Reference number: A48149; MUID:93180797; PMID:8382772  
A;Accession: B48149  
A;Molecule type: DNA  
A;Residues: 1-314 <LN>  
A;Cross-references: GB:MM3011; PIDN:AAA35861.1; PID:9182996  
A;Experimental source: colorectal carcinoma cell line SW948  
R;Simon, B.; Podolny, D.K.; Moldenhauer, G.; Isabellbacher, K.J.; Gattoni-Celli, S.; Branc  
Proc. Natl. Acad. Sci. U.S.A. 87, 3542-3546, 1990  
A;Title: Molecular cloning of cDNA for the carcinoma-associated antigen GA733-2.  
A;Reference number: A35907; MUID:90239051; PMID:2333300  
A;Accession: A5907  
A;Molecule type: mRNA  
A;Residues: 1-314 <SZA>  
A;Cross-references: GB:MM3011; PIDN:AAA35861.1; PID:9182996  
A;Experimental source: colorectal carcinoma cell line SW948  
R;Strnad, J.; Hamilton, A.E.; Beavers, L.S.; Gamboa, G.C.; Apelgren, L.D.; Taber, L.D.;  
Cancer Res. 49, 314-317, 1989  
A;Title: Molecular cloning and characterization of a human adenocarcinoma/epithelial cell  
A;Reference number: A37377; MUID:90089370; PMID:2463074  
A;Accession: A37377  
A;Molecule type: mRNA  
A;Residues: 1-276 'M', 278-314 <STR>  
A;Cross-references: GB:MM32325; PIDN:9186775; PID:9307091  
A;Experimental source: R;Perez, M.S.; Walker, L.E.  
J. Immunol. 142, 3662-3667, 1989  
A;Title: Isolation and characterization of a cDNA encoding the KS1/4 epithelial carcinoma  
A;Reference number: A45898; MUID:89235177; PMID:2469722  
A;Molecule type: mRNA  
A;Residues: 1-276 'M', 278-314 <PER>  
A;Cross-references: GB:MM26481; PIDN:91619789; PIDN:AAA9543.1; PID:9619790  
R;Durbin, H.; Rodrigues N.; Bodmer, W.F.  
Int. J. Cancer 45, 552-565, 1990  
A;Title: Further characterization, isolation and identification of the human adenocarcinoma-associated glycoprotein  
A;Reference number: A60298; MUID:20170210; PMID:2307344  
A;Accession: A60298  
A;Molecule type: protein  
A;Residues: 82-98 <DUR>  
A;Experimental source: normal colonic mucosa  
R;Sportsman, J.R.; Taber, L.D.; Slisz, M.C.; Apelgren, L.D.; Bumol, T.F.  
Biotechnol. Appl. Biochem. 10, 516-544, 1988  
A;Title: Isolation and characterization of the human adenocarcinoma-associated glycoprotein  
A;Reference number: A61569; MUID:89166093; PMID:3069116  
A;Accession: A61569  
A;Molecule type: protein  
A;Residues: 82-97 <SPO>  
C;Superfamily: epithelial glycoprotein antigen GA733: EGF homology; thyroglobulin type I  
C;Keywords: glycoprotein; intestine; transmembrane protein  
F;1-23/Domain: signal sequence #status predicted <PRO>  
F;24-81/Domain: propептид #status predicted <PRO>  
R;Sportsman, J.R.; Taber, L.D.; Slisz, M.C.; Apelgren, L.D.; Bumol, T.F.  
F;66-135/Domain: thyroglobulin type I repeat homology <THY1>  
F;82-214/Domain: epithelial glycoprotein antigen GA733-2 #status predicted <MAT>  
F;82-265/Domain: extracellular #status predicted <EXT>  
F;266-288/Domain: transmembrane #status predicted <INT>  
F;289-311/Domain: intracellular #status predicted <INT>  
F;7,111,198/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 96.4%; Score 27; DB 2; Length 314;

Best Local Similarity 83.3%; Pred. No. 72; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEXGLF 6  
Db 100 DESGLF 105

**RESULT 6**  
jerky gene protein homolog - human  
C;Species: Homo sapiens (man)  
C;Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: JCS594  
R;Zhang, Z.; Kyaw, H.; Gakenheimer, K.R.; Augustus, M.; Fan, P.; Zhang, X.; Su, K.; Carte Biochem. Biophys. Res. Commun. 236, 389-395, 1997  
A;Title: Cloning, mapping and tissue distribution of a human homologue of the mouse jerky gene  
A;Reference number: JCS594; MUID:97382443; PMID:9240447  
A;Accession: JCS594  
A;Molecule type: mRNA  
A;Residues: 1-442 <ZEN>  
A;Cross-references: UNIPROT:Q9Y4A0; DDBJ:AF0047428; PIDN:AAB65833.1; PMID:92314628  
A;Note: it is uncertain whether Met-1 or Met-33 is the initiator  
C;Comment: This protein functions as a nuclear regulatory protein.  
C;Genetics:  
A;Gene: hhnjg  
A;Map position: 11q21

Query Match 96.4%; Score 27; DB 2; Length 442;  
Best Local Similarity 83.3%; Pred. No. 1e+02; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEXGLF 6  
Db 95 DESGLF 100

**RESULT 7**  
AG3139  
flavin-containing monooxygenase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C;Accession: AG3139  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCellen, J.; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A;Author: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, M.; Kamm, B.W.  
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; MUID:21608550; PMID:11743193  
A;Status: preliminary  
A;Molecule type: DNA  
A;Cross-references: UNIPROT:Q8U6R8; GB:AB008689; PIDN:AAL45533.1; PMID:917743245; GSPDB:CA;Experiment 1 source: strain C58 (Dupont)  
A;Genes: Atu4739  
A;Map position: linear chromosome

Query Match 96.4%; Score 27; DB 2; Length 469;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEXGLF 6  
Db 310 DESGLF 315

**RESULT 8**  
JE0225  
JH8 protein - human

C;Species: Homo sapiens (man)  
C;Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 17-Mar-1999  
C;Accession: JE0225  
R;Morita, R.; Miyazaki, B.; Fong, C.G.; Chen, X.N.; Korenberg, J.R.; Delgado-Eskena, A.V.  
A;Title: JH8, a gene highly homologous to the mouse jerky gene, maps to the region for cl  
A;Reference number: JE0225  
A;Accession: JE0225  
A;Molecule type: mRNA  
A;Residues: 1-320 <ZOR>  
A;Experimental source: brain  
A;Note: homologous to mouse jerky protein  
A;Gene: JH8  
A;Map position: 8q24.3

Query Match 96.4%; Score 27; DB 2; Length 520;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEXGLF 6  
Db 139 DETGLF 144

**RESULT 9**  
E98148  
hypothetical protein AGR\_L\_284 [imported] - Agrobacterium tumefaciens (strain C58, Cereor  
C;Species: Agrobacterium tumefaciens  
C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C;Accession: E98148  
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens  
A;Reference number: A97359; MUID:21608551; PMID:11743194  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-605 <ZUR>  
A;Cross-references: UNIPROT:Q8U6R8; GB:AE007870; PIDN:AAK88711.1; PMID:915158447; GSPDB:GN  
C;Genetics:  
A;Gene: AGR\_L\_284  
A;Map position: linear chromosome

Query Match 96.4%; Score 27; DB 2; Length 605;  
Best Local Similarity 83.3%; Pred. No. 1.4e+02; Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEXGLF 6  
Db 446 DESGLF 451

**RESULT 10**  
E97630  
hypothetical protein AGR\_C\_4105 [imported] - Agrobacterium tumefaciens (strain C58, Cereor  
C;Species: Agrobacterium tumefaciens  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: E97630  
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quollo, B.; Goldman, A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens  
A;Reference number: A97359; MUID:21608551; PMID:11743194  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-654 <ZUR>  
A;Cross-references: UNIPROT:Q8UD70; GB:AE007869; PIDN:AAK87998.1; PMID:915157412; GSPDB:GN  
C;Genetics:  
A;Gene: AGR\_C\_4105  
A;Map position: circular chromosome

Query Match 96.4%; Score 27; DB 2; Length 694;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEXGLF 6  
 Db 576 DETGLF 581

RESULT 11  
 AHz853 conserved hypothetical protein Atu2257 [Imported] - Agrobacterium tumefaciens (strain C5  
 C;Species: Agrobacterium tumefaciens  
 C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
 C;Accession: AH2853  
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Erate, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.  
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A;Reference number: AB2577; MUID:21608550; PMID:11743193  
 A;Accession: AH2853  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-694 <KUR>  
 A;Cross-references: UNIPROT:Q8UD70; GB:AE008688; PIDN:AAI43246.1; PID:917740731; GSPDB:G  
 A;Experimental source: strain C58 (Dupont)  
 C;Genetics:  
 A;Gene: Atu2257  
 A;Map position: circular chromosome

Query Match 96.4%; Score 27; DB 2; Length 694;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02; Indels 0; Mismatches 1; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEXGLF 6  
 Db 576 DETGLF 581

RESULT 12  
 C89786 hypothetical protein SA0224 [Imported] - Staphylococcus aureus (strain N315)  
 C;Species: Staphylococcus aureus  
 C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
 C;Accession: C89786  
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
 Lancet 357, 1225-1240, 2001  
 A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.  
 A;Accession: C89786  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-753 <KUR>  
 A;Cross-references: UNIPROT:Q99WZ1; GB:BA000018; PID:g13700147; PIDN:BAB41446.1; GSPDB:G  
 A;Experimental source: strain N315  
 C;Genetics:  
 A;Gene: SA0224

Query Match 96.4%; Score 27; DB 2; Length 753;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02; Indels 1; Mismatches 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 DEXGLF 6  
 Db 334 DEAGLF 339

RESULT 13  
 PYFG parvalbumin beta - edible frog  
 C;Species: Rana esculenta (edible frog)  
 C;Date: 30-Nov-1980 #text\_change 09-Jul-2004  
 C;Accession: A03052  
 R;Capony, J.P.; Demaillé, J.; Pina, C.; Pechere, J.F.  
 Eur. J. Biochem. 56, 215-227, 1975  
 A;Title: The amino-acid sequence of the most acidic major parvalbumin from frog muscle.  
 A;Reference number: A03052; MUID:76022442; PMID:10807077  
 A;Accession: A03052  
 A;Molecule type: protein  
 A;Residues: 1-108 <CAP>  
 A;Cross-references: UNIPROT:PO2617; UNIPROT:Q8J1U1  
 A;Note: the isoelectric point of this protein is 4.5  
 C;Superfamily: parvalbumin; calmodulin repeat homology  
 C;Keywords: blocked amino end; calcium binding; duplication; EF hand; muscle  
 F:38-70/Domain: calmodulin repeat homology <EF1>  
 F:77-108/Domain: calmodulin repeat homology <EF2>  
 F:1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental  
 F:51-53, 55-57, 59-62/Binding site: calcium (Asp, Asp, Ser, Phe, Glu, Glu) #status predicted  
 F:90, 92, 94, 96, 101/Binding site: calcium (Asp, Asp, Asp, Lys, Glu) #status predicted

Query Match 92.9%; Score 26; DB 1; Length 108;  
 Best Local Similarity 83.3%; Pred. No. 43;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEXGLF 6  
 Db 61 DELGLF 66

RESULT 14  
 A69932 hypothetical protein yozM - Bacillus subtilis  
 C;Species: Bacillus subtilis  
 C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C;Accession: A69932  
 R;Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 398, 241-256, 1997  
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleri, J.; Harwood, C.R.; Hennet, A.; Hilbert, H.; Hobappel, S.; Hobono, S.; Hull, M.P.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lardinois, Y.M.; Ogawa, K.; Ogiwara, A.; Ono, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel, Rieger, M.; Rivolta, C.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A;Authors: Schleicher, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, Akenouchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Togoni, A.; Totsuka, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshihara, A.; Authors: Yoshihara, H.F.; Zumstein, E.; Yoshihara, H.; Danchin, A.  
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A;Reference number: A69932; MUID:98044033; PMID:9384377  
 A;Accession: A69932  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Genes: yozM

Query Match 92.9%; Score 26; DB 2; Length 111;  
 Best Local Similarity 83.3%; Pred. No. 45;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEXGLF 6  
 Db 39 DERGLF 44

G71880  
hypothetical protein Jhp0852 - Helicobacter pylori (strain J99)  
C;Species: Helicobacter pylori  
A;Variety: strain J99  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: G71880  
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen  
A;Reference number: A718000, MUID:9923682  
A;Accession: G71880  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-143 <ARN>  
A;Cross-references: UNIPROT:Q92XK3; GB:AE001514; GB:AE001439; NID:94155418; PMID:AA00643  
A;Experimental source: strain J99  
C;Genetics:  
A;Gene: Jhp0852

Query Match 92.9%; Score 26; DB 2; Length 143;  
Best Local Similarity 83.3%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 DEXGLF 6  
|||  
Db 119 DEXGLF 124

Search completed: January 3, 2005, 13:53:03  
Job time : 39 secs







PT hyperproliferative disorders and autoimmune disorders.

XX Disclosure: SEQ ID NO 10; 1037pp; English.

PA (KUFE/) KUFEER P.

PA (RAUM/) RAUM T.

XX PI Kufner P, Raum T;

XX DR WPI; 1998-594564/50.

PT Production of anti-human antigen receptors - by selecting a combination of functionally rearranged VH and VL immunoglobulin chains expressed from a recombinant vector.

XX PS Example 5; Page 40; 84pp; English.

CC This is the amino acid sequence of a synthetic peptide used in the method of the invention, involving the identification of receptors that can be used for targeting antigens in humans without being immunogenic themselves. Such receptors can be used for treating diseases such as tumours or auto-immune diseases, graft rejection after transplantation, infectious diseases by targeting cellular receptors as well as allergic, inflammatory, endocrine and degenerative diseases by targeting key molecules involved in the pathological process

XX Sequence 13 AA;

Query Match 96.4%; Score 27; DB 2; Length 13;

Best Local Similarity 83.3%; Pred. No. 9.4;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX SQ

QY 1 DEXGLF 6

Db 6 DESGLF 11

RESULT 5

ID ABP00014 standard; protein; 66 AA.

AC ABP00014;

XX DT 25-JUN-2002 (first entry)

XX DB Human ORFX protein sequence SEQ ID NO:10.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester deficiency; immune deficiency; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis; graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis.

XX SQ reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).

QY 1 DEXGLF 6

Db 45 DEAGLF 50

RESULT 6

ID AAO19722 standard; protein; 76 AA.

AC AAO19722;

XX DT 10-APR-2003 (first entry)

XX Human GA733-2 protein thyroglobulin domain.

XX Human; epithelial glycoprotein; mGCP; immune response suppression; tumour-associated antigen; gene therapy; autoimmune disorder; immunosuppressive; antiinflammatory; neuroprotective; antihaemetic; antiarthritic; dermatological; antiinflammatory; antianæmic.

XX OS Homo sapiens.

XX PN WO20192523-A2.

XX PD 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US010936.

XX PP 30-MAY-2000; 2000US-0206132P.

PR 29-AUG-2000; 2000US-0228716P.

XX (CURA-) CURAGEN CORP.

PA Shimkets RA, Leach MD;

XX PI XX

XX Eck SL;

XX DR WPI; 2003-167107/16.

DR N-PSDB; ABZ20937.

PT Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, PT

XX Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, PT

PT Modulating an undesirable immune response, e.g. transplant rejection, in PT

PT patients, comprises administering a composition comprising a tumor-  
 XX associated antigen molecule in a carrier to the patient.  
 PS Claim 15; Fig 15; 87pp; English.  
 XX

The present invention relates to a method of modulating an undesirable  
 CC immune response in a recipient host mammal to enhance tolerance in the  
 recipient, which comprises administering at least one composition  
 comprising a tumor-associated antigen molecule in a carrier to the  
 recipient host mammal, in an amount to modulate the undesirable immune  
 CC responses. The method is useful in suppressing undesirable immune  
 responses in humans which may lead to a disorder such as diabetes,  
 transplant rejection, multiple sclerosis, rheumatoid arthritis, systemic  
 CC lupus erythematosus, or pernicious anemia. The nucleic acids and  
 proteins identified in the invention may be used in screening assays to  
 assess agents that modulate tumour-associated antigen mediated regulation  
 CC of antigen recognition and immune suppression, as research tools to  
 identify other proteins that are involved in antigen presentation by  
 Major Histocompatibility Complex (MHC) Class II molecules, and in various  
 CC diagnostic and therapeutic applications (e.g. in treating the above-  
 mentioned diseases). The present sequence is the thyroglobulin domain of  
 the human tumour-associated antigen GA733-2 sequence shown in the  
 CC exemplification of the invention

XX Sequence 76 AA;

Query Match 96.4%; Score 27; DB 6; Length 76;  
 Best Local Similarity 83.3%; Pred. No. 62;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 DEXGLF 6  
 Db 38 DESGLF 43

RESULT 7  
 ID AAY95248 Standard; peptide; 106 AA.  
 XX  
 AAY95248;  
 XX 29-AUG-2000 (First entry)  
 XX  
 DE Colorectal cancer antigen GA733-2.  
 XX  
 KW Colorectal cancer; antigen; GA733-2; virus infected plant; vaccine;  
 PN PNF1/TVE; alfalfa mosaic virus; transcomplementation.  
 XX  
 Homo sapiens.  
 PN W0200025574-A1.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 29-OCT-1999; 99WO-US025566.  
 XX  
 PR 30-OCT-1998; 98US-0106221P.  
 PA (UYE-) UNIV JEFFERSON THOMAS.  
 XX  
 PI Koprowski H, Yusibov V;  
 XX  
 DR WPI; 2000-365296/31.

XX Producing full-length antibody in a host plant for use as vaccines,  
 PT involves using recombinant viral vectors or transcomplementation systems.  
 XX  
 Example 1; Fig 1B; 87pp; English.  
 XX  
 This peptide is colorectal cancer antigen GA733-2, which is recognised  
 CC by colorectal cancer associated antigen 17-<sup>1A</sup>. GA733-2 was fused with the  
 CC coat protein of alfalfa mosaic virus (AlMV), and the fusion product was  
 CC cloned into full-length RNA3 of AlMV to create PNF1/TVE. This construct

CC can be used to express GA733-2 in infected plants. In construct PNF2/TVE,  
 CC non-full-length AlMV coat protein is used. The invention discloses novel  
 CC methods for producing foreign polypeptides in a host plant using  
 CC recombinant viral vectors, such as AlMV, and transcomplementation  
 CC systems. The products expressed in the plant can be used as vaccine  
 CC components or in other biomedical applications  
 XX Sequence 106 AA;  
 SQ  
 Query Match 96.4%; Score 27; DB 3; Length 106;  
 Best Local Similarity 83.3%; Pred. No. 89;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 DEXGLF 6  
 Db 85 DESGLF 90

RESULT 8  
 ID ABG13551 Standard; protein; 107 AA.  
 XX  
 AC ABG13551;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #13542.  
 XX  
 Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 XX  
 food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 Homo sapiens.  
 OS  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PR 30-MAR-2001; 2001WO-US000631.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 XX  
 PR 23-AUG-2000; 2000US-00649167.  
 XX  
 PA (HYSEQ-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 WPI; 2001-639362/73.  
 DR N-PSDB; AS77738.

XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 20; SEQ ID NO 43910; 103pp; English.  
 XX  
 The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG0010-ABG3037 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)

SQ Sequence 107 AA;  
 Query Match 96.4%; Score 27; DB 4; Length 107;  
 Best Local Similarity 83.3%; Pred. No. 90;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 DEXGLP 6  
 Db 100 DESGLF 105

RESULT 9  
 AAO01704 06-NOV-2001 (first entry)  
 ID AAO01704 Human polypeptide SEQ ID NO 15596.  
 XX DE Human; cycokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haemopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.  
 OS Homo sapiens.  
 XX AC AAO01704;  
 XX DT WO200164835-A2.  
 XX DT 07-SEP-2001.  
 XX PR 26-FEB-2001; 2001WO-US004927.  
 XX PR 28-FEB-2000; 2000US-00515126.  
 XX PR 18-MAY-2000; 2000US-00577409.  
 XX PA (HYSB-) HYSBQ INC.  
 XX PI Tang YT, Liu C, Drmanac RT;  
 XX DR WPI: 2001-514838/56.  
 XX DR -PSDB, AAI181635.

PT Isolated nucleic acids and polypeptides, useful for preventing, diagnosing  
 PT and treating e.g. leukemia, inflammation and immune disorders.  
 XX Claim 20; SEQ ID NO 15596; 1399pp + Sequence Listing; English.  
 PS The invention relates to human polynucleotides (AAI79941-AAI93841) and  
 XX the encoded proteins (AA000010-AA013910) that exhibit activity relating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and peptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The Polypeptides have various cytokine-like activities,  
 e.g. stem cell growth factor activity, haemopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity, and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)  
 XX Sequence 126 AA;

SQ Query Match 96.4%; Score 27; DB 4; Length 126;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX

Qy 1 DEXGLP 6  
 Db 35 DESGLF 40

RESULT 10  
 AAG75962 03-SEP-2001 (first entry)  
 ID AAG75962 Human colon cancer antigen protein SEQ ID NO 6726.  
 XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KW colorectal carcinoma; chromosome 4.  
 XX DE Human colon cancer antigen protein SEQ ID NO 6726.  
 XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KW colorectal carcinoma; chromosome 4.  
 XX OS Homo sapiens.  
 XX PN WO200122920-A2.  
 XX PD 05-APR-2001.  
 XX PF 28-SEP-2000; 2000WO-US026524.  
 XX PR 29-SEP-1999; 99US-0157137P.  
 XX PR 03-NOV-1999; 99US-0163280P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Ruben SM, Barash SC, Birse CB, Rosen CA;  
 XX DR WPI: 2001-235357/24.  
 XX DR -PSDB, AAI35367.

RESULT 11

Qy 1 DEXGLP 6  
 Db 88 DESGLF 93

ADP81219 ID ADP81219 standard; protein; 240 AA. XX	Db 100 DESGLF 105
AC ADP81219; XX	RESULT 12 AD143131 ID AD143131 standard; protein; 244 AA. XX
DT 09-SEP-2004 (first entry)	AC AD143131; XX
DE Protein of human ovarian specific gene, SEQ ID No 253.	DT 22-APR-2004 (first entry)
XX	DE Plant transcription factor #541.
KW normal; neoplastic; ovarian; ovarian specific nucleic acid; OSNA;	XX
KW metastatic; cancer; vaccine; cytostatic; human.	XX
XX	XX
OS Homo sapiens.	DE Plant transcription factor #541.
PN WO2004053079-A2.	XX
XX	KW transgenic; plant; enhanced tolerance to abiotic stress;
PD 24-JUN-2004.	XX
XX	KW glyphosphate tolerance; hormone sensitivity; disease resistance;
PR 08-DEC-2003; 2003WO-US038855.	XX
XX	KW sugar sensing; flowering; flower structure; stem bifurcation;
PR 06-DEC-2002; 2002US-0431301P.	XX
PR 06-DEC-2002; 2002US-0431301P.	XX
PR 30-JUN-2003; 2003US-0484584P.	XX
PR 07-NOV-2003; 2003US-0518607P.	XX
PA (DIAD-) DIADEXUS INC.	OS Oryza sativa.
XX	XX
PI Macina RA, Turner LR, Sun Y, Liu S, Chen H;	PN US2004019927-A1.
XX	XX
WPI: 2004-468850/44.	PD 29-JAN-2004.
DR N-PSDB; ADP81060.	XX
XX	PP 25-FEB-2003; 2003US-00374780.
PT New ovarian specific nucleic acid molecules and polypeptides useful for	XX
PT diagnosing, preventing or treating ovarian cancer, for producing	XX
PT transgenic animals or cells, or for research purposes.	PR 18-APR-2001; 2001US-00837944.
XX	XX
PS Claim 12; SEQ ID NO 253; 754pp; English.	PA (SHERMAN B K., SHERMAN B K., PA (RIECHMANN J L., RIECHMANN J L., PA (JIAN C., JIANG C., PA (HEAR J E., HEARD J E., PA (HAAK V., HAAKE V., PA (CREE R A., CREEMLAN R A., PA (RATCLIFFE O., RATCLIFFE O., PA (ADAM L J., ADAM L J., PA (REUBER T L., REUBER T L., PA (KEDDIE J., KEDDIE J., PA (BROWN P E., BROWN P E., PA (PILGRAM M L., PILGRAM M L., PA (DUBELL A N., DUBELL A N., PA (PINEDA O., PINEDA O., PA (YU G., YU G., PA (XX
CC The invention relates to novel isolated nucleic acid molecules and	XX
CC polypeptides present in normal and neoplastic ovarian cells. These	XX
CC comprise a nucleic acid sequence encoding any of the 167 amino acid	XX
CC sequences (e.g. 438, 237 or 233 amino acids) fully defined in the	XX
CC specification (SEQ ID Nos: ADP81095 to ADP81161) and comprises any of	XX
CC the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined	XX
CC in the specification (SEQ ID Nos: ADP80367 to ADP81094). The invention	XX
CC further comprises: a method for determining the presence of a ovarian	XX
CC specific nucleic acid (OSNA) in a sample; a vector comprising the above	XX
CC nucleic acid molecule; a host cell comprising the vector; a method for	XX
CC producing a polypeptide encoded by the above nucleic acid molecule; a	XX
CC polypeptide encoded by the nucleic acid molecule cited above; an antibody	XX
CC method for determining the presence of the above polypeptide; a	XX
CC sample; a method for diagnosing or monitoring the presence and metastases	XX
CC of ovarian cancer in a patient; a kit for detecting a risk of cancer or	XX
CC determining the presence of the above nucleic acid molecule or	XX
CC polypeptide; a method of treating a patient with ovarian cancer; and a	XX
CC vaccine comprising the above polypeptide or nucleic acid encoding the	XX
CC polypeptide. The isolated nucleic acid molecules and polypeptides have	XX
CC cytostatic activity. The isolated polypeptides may be used to create a	XX
CC vaccine. The isolated nucleic acid molecules and polypeptides can be used	XX
CC for diagnosing or monitoring the presence and metastases of ovarian	XX
CC cancer and treating ovarian cancer. This sequence represents the protein	XX
CC of an ovarian specific gene of the invention.	XX
SQ Sequence 240 AA;	XX
Score 27; DB 8; Length 240;	XX
Best Local Similarity 96.4%; Pred. No. 2.1e+02;	XX
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	XX
Qy 1 DEXGLF 6	XX

CC premature senescence; increased necrosis; increase in seedling or plant size; decreased plant size; leaf morphology; seed morphology; seed biochemistry; increase in root anthocyanins; increase in Plant anthocyanins; or alteration in light response or shade avoidance. The transgenic plant, polynucleotides and polypeptides are useful in bioinformatic search methods. This is the amino acid sequence of a plant transcription factor, and an orthologue of *Arabidopsis thaliana* transcription factors isolated in the invention, that can be used in the creation of a transgenic plant with altered traits.

Sequence 244 AA;  
 Query Match 96.4%; Score 27; DB 8; Length 244;  
 Best Local Similarity 93.3%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 DEXGLF 6  
 Db 26 DEAGLF 31

RESULT 13  
 ADO03227 ID ADO03227 Standard; protein; 244 AA.  
 AC ADO03227;  
 XX DT 01-JUN-2004 (first entry)

XX Thalecress transcription factor, Rice orthologue #126.

DE Rice; transcription factor; plant; transgenic; abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress; phosphate limitation; potassium limitation; nitrogen limitation; hormone sensitivity; disease resistance; sugar sensing; seed germination; flowering; inflorescence architectural change; meristem cell differentiation; phyllotaxy; apical dominance; trichome development; seed development; premature senescence; delayed senescence; lethality; necrosis; plant size; leaf morphology; seed morphology; secondary metabolism; light response; shade avoidance. Oryza sativa.

OS PN US2004045049-A1.

PD 04-MAR-2004.

PP 10-APR-2003; 2003US-00412699.  
 XX 13-SEP-1999; 99US-00394519.  
 PR 21-JAN-2000; 2000US-00489376.  
 PR 17-FEB-2000; 2000US-00506720.  
 PR 22-MAR-2000; 2000US-00532991.  
 PR 22-MAR-2000; 2000US-00533029.  
 PR 22-MAR-2000; 2000US-00533040.  
 PR 22-MAR-2000; 2000US-00533392.  
 PR 22-MAR-2000; 2000US-00533448.  
 PR 06-APR-2000; 2000WO-08009448.  
 PR 16-NOV-2000; 2000US-00713994.  
 PR 27-MAR-2001; 2001US-00819142.  
 PR 17-APR-2001; 2001US-00837444.  
 PR 30-JAN-2002; 2002US-00958131.  
 PR 14-JUN-2002; 2002US-00171468.  
 PR 09-AUG-2002; 2002US-00225066.  
 PR 09-AUG-2002; 2002US-00225067.  
 PR 09-AUG-2002; 2002US-00225068.  
 PR 17-DEC-2002; 2002US-0434165P.  
 PR 25-FEB-2003; 2003US-00374780.

XX (ZHAN) ZHANG J.  
 PA (FROM) FROM M. E.  
 PA (HEAR) HEARD J. E.  
 PA (RIEC) RIECHMANN J. L.

PA (ADAM) ADAM L. J.  
 PA (BROW) BROWN P. E.  
 PA (PINE) PINEDA O.  
 PA (REUB) REUBER T. L.  
 PA (KEDD) KEDDIE J. S.  
 PA (YUGG) YU G.  
 PA (JIAN) JIANG C.  
 PA (SAM) SAMAH R. S.  
 PA (PILG) PILGRIM M. L.  
 PA (CRE) CREELMAN R. A.  
 PA (DUBB) DUBELL A. N.  
 PA (RATC) RAYCLIFFE O.  
 PA (KUM) KUMIMOTO R.  
 PA (SHER) SHERMAN B. K.  
 XX  
 PA Zhang J., Fromm ME, Heard JE, Riechmann JL, Adam L., Brown PE; Pineda O., Reuber TL, Keddie JS, Yu G., Jiang C., Samaha RS; Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O., Kumimoto R.; Sherman BK; XX  
 XX  
 DR WPI; 2004-225755/21.  
 XX  
 XX New transgenic plant, useful in developing phenotypes with altered or improved characteristics or traits.  
 XX  
 PS Claim 1; SEQ ID NO 1641; 213pp; English.  
 XX  
 XX The invention relates to a transgenic plant comprising a recombinant polynucleotide having a polynucleotide sequence or its complementary sequence comprising a sequence encoding polypeptide, that initiates transcription (i.e. a transcription factor) from *Arabidopsis*, *Soybean*, *Rice*, *Rape* or *Corn*, comprising any of the sequences appearing as ADO01588-ADO03527 or ADO03530-ADO03559. Also included are using transgenic plant to grow a progeny plant, an expression cassette comprising a constitutive, inducible or tissue-specific promoter and a recombinant polynucleotide described above), a host cell comprising the expression cassette, producing a modified plant having a modified trait, identifying a factor that is modulated by or interacts with a polypeptide encoded by the polynucleotide sequence and identifying at least one downstream polynucleotide sequence that is subject to a regulatory effect of any of the polypeptides encoded by the polynucleotide described above. The transgenic plant is useful for producing a plant that has an altered trait e.g. an enhanced tolerance to abiotic stress (increased tolerance to chilling, germination in cold conditions freezing tolerance, tolerance to heat, tolerance to drought, tolerance to osmotic stress, tolerance to salt, tolerance to phosphate limitation, tolerance to potassium limitation, decreased sensitivity to nitrogen limitation), altered hormone sensitivity, reduced sensitivity to abscisic acid, an altered response to ethylene, disease resistance, altered susceptibility to Botrytis, altered susceptibility to Fusarium, altered susceptibility to *Erysiphe*, altered susceptibility to *Pseudomonas syringae*, altered susceptibility to *Sclerotinia*, altered sugar sensing, improved seed germination and seedling vigor, early flowering, late flowering, extended period of flowering, an inflorescence architectural change, a change in stem bifurcations, a lack of a shoot meristem, reduced meristem cell differentiation, altered phyllotaxy, altered branching pattern, reduced apical dominance, reduced trichome density, ectopic trichome development, altered trichome development, altered stem morphology, increased root growth, increased root hairs, altered seed shape, delayed cell proliferation/cell differentiation, premature senescence, delayed senescence, lethality, increased necrosis, an increase in seedling or plant size, decreased plant size, a change in leaf morphology, increased leaf development, increased leaf size and mass, glossy leaves, leaf cell expansion, change in seed morphology, altered seed coloration, increased seed size, decreased seed size, altered seed shape, change in leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid content, increased leaf insoluble sugars, decreased leaf insoluble sugars, increased leaf anthocyanins, an alteration of leaf fatty acid content, an alteration of leaf glucosinolate content, change in seed biochemistry, an increase in seed oil content, decrease in seed oil content, increase in seed fatty acid content, decrease in seed fatty acid content, increase in seed protein content, decrease in seed protein content, alteration in seed prenyl lipid content, increase in seed

sterols, upregulation of genes involved in secondary metabolism, increase in root anthocyanins, increase in plant anthocyanins, and alterations in light response or shade avoidance. The present sequence represents an orthologue of a thalectless transcription factor isolated from Rice.

Sequence 244 AA;  
 Query Match 96.4%; Score 27; DB 8; Length 244;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 DEXGLF 6  
 Db 26 DEAGLF 31

RESULT 14  
 AAR36397 standard; protein; 265 AA.  
 XX  
 AC AAR36397;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 09-JAN-2003 (revised)  
 DT 20-AUG-1993 (first entry)  
 XX  
 DB Truncated GA733-2E soluble variant of type I membrane protein.  
 XX  
 GA733-2F; secretory protein; mutant; cancer; immunotherapy; tumour.  
 XX  
 Homo sapiens.  
 PN W09308298-A1.  
 XX  
 PD 29-APR-1993.  
 XX  
 PR 08-OCT-1992; 92WO-US008572.  
 XX  
 PR 18-OCT-1991; 91US-00778232.  
 XX  
 PA (WIST-) WISTAR INST ANATOM & BIOLOGY.  
 XX  
 Linnenbach AJ, Koprowski H, Herlyn D;  
 XX  
 WPI; 1993-152489/18.  
 DR AAQ1176.

Soluble variants of type I membrane protein, GA733-2E and GA733-2F - useful for cancer immuno:therapy and detection of tumour cells.  
 XX  
 Claim 1; Fig 1; 66pp; English.  
 XX  
 Oligonucleotide primers were synthesised for the PCR synthesis of a truncated cDNA that encoded the amino terminal signal peptide and extracellular 212 of the selected antigen, GA733-2. The synthetic primers correspond to nucleotides 85-114 (sense strand) and 885-919 (antisense strand) of the native GA733-2 DNA. The primers were used in standard PCR using GA733-2 cDNA as template. Pharmaceutical compounds, cong. GA733-2B are useful as vaccines for active immunotherapy against carcinomas, and as reagent for detecting GA733-2 antigens expressed on tumour cells. (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)

Sequence 265 AA;  
 Query Match 96.4%; Score 27; DB 2; Length 265;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEXGLF 6  
 Db 100 DESGLF 105

RESULT 15  
 ADL23185 standard; protein; 265 AA.  
 ID ADL23185  
 AC ADL23185;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 Human soluble EP-CAM.  
 XX  
 KW Human; bactericidal/permability-increasing protein; BPI; EP-CAM; CAB2.1; recombinant polypeptide production; ING-1; antibody; anti-CD18 antibody; cosmetic product.

XX  
 Homo sapiens.  
 OS Synthetic.  
 XX  
 US2003203447-A1.  
 XX  
 PD 30-OCT-2003.  
 XX  
 PF 31-MAR-2003; 2003US-00404724.  
 XX  
 PR 29-MAR-2002; 2002US-0368530P.  
 XX  
 PA (HORNW/) HORWITZ A H.  
 XX  
 PI Horwitz AH;  
 XX  
 DR WPI; 2003-875646/81.  
 XX  
 DR N-PSDB; ADL23184.

Producing recombinant polypeptide, useful for treating or diagnosing diseases or conditions, comprising culturing cells transformed or transfected with a vector comprising multiple copies of a transcription unit separated by a selective marker gene.  
 XX  
 Example 12; SEQ ID NO 58; 133pp; English.  
 XX  
 The invention relates to producing a recombinant polypeptide comprising culturing cells, which have been transformed or transfected with a vector, or its segment comprising multiple copies of a transcription unit separated by at least one selective marker gene, where the transcription unit encodes a polypeptide under selective conditions. Also included are a vector or segment comprising multiple copies of a transcription unit separated by at least one selective marker gene where the transcription unit encodes a polypeptide, a host cell comprising an expression vector or segment and a stable cell line comprising an expression vector or segment. Each transcription unit is under the control of its own promoter and 3' untranslated region, where the promoter is an SV40, HSV, bovine growth hormone/thymidine kinase, MPSV, mouse beta Globin, human EF1, MSV -LTR, RSV, MMTV-LTR, CMV, MLV, Chinese hamster elongation factor or mouse Abelson LTR promoter. The expression vector further comprises multiple enhancers. The transcription unit also encodes two different subunits of a multimeric protein, an immunoglobulin light and heavy chain polypeptides or at least the variable regions of the immunoglobulin light and heavy chain polypeptides. It further encodes a BPI protein. The protein product BPI protein fragment, BPI analogue, BPI variant or BPI-derived peptide. The transcription unit encodes an rBPI21 and is under the control of an HCMV promoter and mouse light chain 3' untranslated region, where the vector further comprises 0, 1 or 2 copies of human heavy chain enhancer and either a gpt or neo gene. Other genes suitable for expression using the method of the invention are EP-CAM and CAB2.1 (both not defined). The immunoglobulin may be the ING-1, chimaeric mouse/human antibody (or humanised version or proline substitution mutants) or an anti-CD18 antibody. The method is useful for producing recombinant polypeptide. Recombinant polypeptide compositions are useful in therapeutic, diagnostic procedures or as tools in preventive medicine. Recombinant polypeptides are also found in a wide array of both health and cosmetic products used to increase the quality of life. Complex polypeptide products are also routinely used in research laboratories

both as end products of analyses and as agents in assays for the study or preparation of other molecules. Advantages of the present invention includes increased recombinant polypeptide production, increased production efficiency, greater control and/or regulation over the qualities of the polypeptide expressed, increased stability of cell lines, and/or decreased costs for materials, reagents and/or other resources. The present sequence represents a protein suitable for expression using the method of the invention.

XX  
SQ Sequence 265 AA:  
Query Match 96.4%; Score 27; DB 7; Length 265;  
Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 DDXGLF 6  
Db 100 DESGLF 105

Search completed: January 3, 2005, 13:49:03  
Job time : 158 secs

